

1646

RAW SEQUENCE LISTING DATE: 05/09/2000
 PATENT APPLICATION: US/09/405,735 TIME: 11:10:38

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\05092000\I405735.raw

4 <110> APPLICANT: Pier, Gerald B.
 6 <120> TITLE OF INVENTION: Methods and Products for Treating
 7 Pseudomonas Infection
 9 <130> FILE REFERENCE: B0801/7155 (HCL)
 11 <140> CURRENT APPLICATION NUMBER: 09/405,735
 12 <141> CURRENT FILING DATE: 1999-09-24
 14 <150> PRIOR APPLICATION NUMBER: US 08/681,838
 15 <151> PRIOR FILING DATE: 1996-07-29
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1		
22 <211> LENGTH: 6129		
23 <212> TYPE: DNA		
24 <213> ORGANISM: Homo Sapiens		
26 <220> FEATURE:		
27 <221> NAME/KEY: CDS		
28 <222> LOCATION: (133)...(4575)		
30 <400> SEQUENCE: 1		
31 aatttgaagc aaatgacatc acaggaggc agagaaaaag ggttgagccgg caggcaccca	60	
32 gagtagtagg tctttggcat taggagctt agccagacg gcccctagcag ggaccccgac	120	
33 gccccgagaga cc atg cag agg tcg cct ctg gaa aag gcc agc gtt gtc tcc	171	
34 Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser		
35 1 5 10		
36 aatggatgtt tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt tttttttt		
37 aaa ctt ttt ttc agc tgg acc aga cca att ttg agg aaa gga tac aga	219	
38 Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg		
39 15 20 25		
40 cag cgc ctg gaa ttg tca gac ata tac caa atc cct tct gtt gat tct	267	
41 Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser		
42 43 30 35 40 45		
44 gct gac aat cta tct gaa aaa ttg gaa aga gaa tgg gat aga gag ctg	315	
45 Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu		
46 50 55 60		
47 gct tca aag aaa aat cct aaa ctc att aat gcc ctt cgg cga tgt ttt	363	
48 Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe		
49 65 70 75		
50 ttc tgg aga ttt atg ttc tat gga atc ttt tta tat tta ggg gaa gtc	411	
51 Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val		
52 80 85 90		
53 acc aaa gca gta cag cct ctc tta ctg gga aga atc ata gct tcc tat	459	
54 Thr Lys Ala Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr		
55 95 100 105		
56 gac ccg gat aac aag gag gaa cgc tct atc gcg att tat cta ggc ata	507	
57 Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile		
58		
59		
60		
61		
62		

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63	110	115	120	125	
65	ggc tta tgc ctt ctc ttt att gtg agg aca ctg ctc cta cac cca gcc				555
66	Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala				
67	130	135	140		
69	att ttt ggc ctt cat cac att gga atg cag atg aga ata gct atg ttt				603
70	Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe				
71	145	150	155		
73	agt ttg att tat aag aag act tta aag ctg tca agc cgt gtt cta gat				651
74	Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp				
75	160	165	170		
77	aaa ata agt att gga caa ctt gtt agt ctc ctt tcc aac aac ctg aac				699
78	Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn				
79	175	180	185		
81	aaa ttt gat gaa gga ctt gca ttg gca cat ttc ttg tgg atc gct cct				747
82	Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro				
83	190	195	200	205	
85	ttg caa gtg gca ctc ctc atg ggg cta atc ttg gag ttg tta cag gcg				795
86	Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala				
87	210	215	220		
89	tct gcc ttc ttt gga ctt ggt ttc ctg ata gtc ctt gcc ctt ttt cag				843
90	Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln				
91	225	230	235		
93	gct ggg cta ggg aga atg atg aag tac aga gat cag aga gct ggg				891
94	Ala Gly Leu Gly Arg Met Met Lys Tyr Arg Asp Gln Arg Ala Gly				
95	240	245	250		
97	aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc				939
98	Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile				
99	255	260	265		
101	caa tct gtt aag gca tac tgc ttg gaa gaa gca atg gaa aaa atg att				987
102	Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile				
103	270	275	280	285	
105	gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat				1035
106	Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr				
107	290	295	300		
109	gtg aga tac ttc aat agc tca gcc ttc ttc tca ggg ttc ttt ttg				1083
110	Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val				
111	305	310	315		
113	gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc				1131
114	Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu				
115	320	325	330		
117	cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg				1179
118	Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala				
119	335	340	345		
121	gtc act cgg caa ttt ccc ttg gct gta caa aca ttg tat gac tct ctt				1227
122	Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu				
123	350	355	360	365	
125	gga gca ata aac aaa ata gag gat ttc tta caa aag caa gaa tat aag				1275
126	Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys				
127	370	375	380		

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129 aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta	1323
130 Thr Leu Glu Tyr Asn Leu Thr Thr Glu Val Val Met Glu Asn Val	
131 385 390 395	
133 aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa	1371
134 Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Lys Ala Lys	
135 400 405 410	
137 caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc	1419
138 Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe	
139 415 420 425	
141 ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat	1467
142 Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn	
143 430 435 440 445	
145 ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga	1515
146 Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly	
147 450 455 460	
149 gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct	1563
150 Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro	
151 465 470 475	
153 tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag	1611
154 Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln	
155 480 485 490	
157 ttt tcc tgg att atg cct ggc acc att aaa gaa aat atc atc ttt ggt	1659
158 Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly	
159 495 500 505	
161 gtt tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa	1707
162 Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln	
163 510 515 520 525	
165 cta gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt	1755
166 Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu	
167 530 535 540	
169 gga gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct	1803
170 Gly Glu Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser	
171 545 550 555	
173 tta gca aga gca gta tac aaa gat gct gat ttg tat tta gac tct	1851
174 Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Asp Ser	
175 560 565 570	
177 cct ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc	1899
178 Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser	
179 575 580 585	
181 tgt gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct	1947
182 Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser	
183 590 595 600 605	
185 aaa atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa	1995
186 Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu	
187 610 615 620	
189 ggt agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag	2043
190 Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln	
191 625 630 635	
193 cca gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt	2091

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194	Pro	Phe	Ser	Ser	Lys	Leu	Met	Gly	Cys	Asp	Ser	Phe	Asp	Gln	Phe
195		640			645							650			
197	agt	gca	gaa	aga	aga	aat	tca	atc	cta	act	gag	acc	tta	cac	cgt
198	Ser	Ala	Glu	Arg	Arg	Asn	Ser	Ile	Leu	Thr	Glu	Thr	Leu	His	Arg
199		655			660							665			
201	tca	tta	gaa	gga	gat	gtc	cct	gtc	tcc	tgg	aca	gaa	aca	aaa	aaa
202	Ser	Leu	Glu	Gly	Asp	Ala	Pro	Val	Ser	Trp	Thr	Glu	Thr	Lys	Gln
203		670			675						680				685
205	tct	ttt	aaa	cag	act	gga	gag	ttt	ggg	gaa	aaa	agg	aag	aat	tct
206	Ser	Phe	Lys	Gln	Thr	Gly	Glu	Phe	Gly	Glu	Lys	Arg	Lys	Asn	Ser
207						690				695			700		
209	ctc	aat	cca	atc	aac	tct	ata	cga	aaa	ttt	tcc	att	gtg	caa	aag
210	Leu	Asn	Pro	Ile	Asn	Ser	Ile	Arg	Lys	Phe	Ser	Ile	Val	Gln	Lys
211						705				710			715		
213	ccc	tta	caa	atg	aat	ggc	atc	gaa	gag	gat	tct	gat	gag	cct	tta
214	Pro	Leu	Gln	Met	Asn	Gly	Ile	Glu	Glu	Asp	Ser	Asp	Glu	Pro	Leu
215						720				725			730		
217	aga	agg	ctg	tcc	tta	gta	cca	gat	tct	gag	cag	gga	gag	gcg	ata
218	Arg	Arg	Leu	Ser	Leu	Val	Pro	Asp	Ser	Glu	Gln	Gly	Glu	Ala	Ile
219						735				740			745		
221	cct	cgc	atc	agc	gtg	atc	agc	act	ggc	ccc	acg	ctt	cag	gca	cga
222	Pro	Arg	Ile	Ser	Val	Ile	Ser	Thr	Gly	Pro	Thr	Leu	Gln	Ala	Arg
223						750				755			760		765
225	agg	cag	tct	gtc	ctg	aac	ctg	atg	aca	cac	tca	gtt	aac	caa	ggt
226	Arg	Gln	Ser	Val	Leu	Asn	Leu	Met	Thr	His	Ser	Val	Asn	Gln	Gly
227						770				775			780		
229	aac	att	cac	cga	aag	aca	aca	gca	tcc	aca	cga	aaa	gtg	tca	ctg
230	Asn	Ile	His	Arg	Lys	Thr	Thr	Ala	Ser	Thr	Arg	Lys	Val	Ser	Leu
231						785				790			795		
233	cct	cag	gca	aac	ttg	act	gaa	ctg	gat	ata	tat	tca	aga	agg	tta
234	Pro	Gln	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Ile	Tyr	Ser	Arg	Arg	Leu
235						800				805			810		
237	caa	gaa	act	ggc	ttg	gaa	ata	agt	gaa	gaa	att	aac	gaa	gac	tta
238	Gln	Glu	Thr	Gly	Leu	Glu	Ile	Ser	Glu	Glu	Ile	Asn	Glu	Glu	Asp
239						815				820			825		
241	aag	gag	tgc	ctt	ttt	gat	gat	atg	gag	agc	ata	cca	gca	gtg	act
242	Lys	Glu	Cys	Leu	Phe	Asp	Asp	Met	Glu	Ser	Ile	Pro	Ala	Val	Thr
243						830				835			840		845
245	tgg	aac	aca	tac	ctt	cga	tat	att	act	gtc	cac	aag	agc	tta	att
246	Trp	Asn	Thr	Tyr	Leu	Arg	Tyr	Ile	Thr	Val	His	Lys	Ser	Leu	Ile
247						850				855			860		
249	gtg	cta	att	tgg	tgc	tta	gta	att	ttt	ctg	gca	gag	gtg	gtc	gtc
250	Val	Leu	Ile	Trp	Cys	Leu	Val	Ile	Phe	Leu	Ala	Glu	Val	Ala	Ala
251						865				870			875		
253	ttg	gtt	gtg	ctg	tgg	ctc	ctt	gga	aac	act	cct	ctt	caa	gac	aaa
254	Leu	Val	Val	Leu	Trp	Leu	Leu	Gly	Asn	Thr	Pro	Leu	Gln	Asp	Lys
255						880				885			890		
257	aat	agt	act	cat	agt	aga	aat	aac	agc	tat	gca	gtg	att	atc	acc
258	Asn	Ser	Thr	His	Ser	Arg	Asn	Asn	Ser	Tyr	Ala	Val	Ile	Ile	Thr

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259	895	900	905	
261	acc agt tcg tat tat gtg ttt tac att tac gtg gga gta gcc gac act			2907
262	Thr Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr			
263	910	915	920	925
265	ttg ctt gct atg gga ttc aga ggt cta cca ctg gtg cat act cta			2955
266	Leu Leu Ala Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu			
267	930	935	940	
269	atc aca gtg tcg aaa att tta cac cac aaa atg tta cat tct gtt ctt			3003
270	Ile Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu			
271	945	950	955	
273	caa gca cct atg tca acc ctc aac acg ttg aaa gca ggt ggg att ctt			3051
274	Gln Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu			
275	960	965	970	
277	aat aga ttc tcc aaa gat ata gca att ttg gat gac ctt ctg cct ctt			3099
278	Asn Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu			
279	975	980	985	
281	acc ata ttt gac ttc atc cag ttg tta att gtg att gga gct ata			3147
282	Thr Ile Phe Asp Phe Ile Gln Leu Leu Leu Val Ile Gly Ala Ile			
283	990	995	1000	1005
285	gca gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg cca			3195
286	Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro			
287	1010	1015	1020	
289	gtg ata gtg gct ttt att atg ttg aga gca tat ttc ctc caa acc tca			3243
290	Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser			
291	1025	1030	1035	
293	cag caa ctc aaa caa ctg gaa tct gaa ggc agg agt cca att ttc act			3291
294	Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr			
295	1040	1045	1050	
297	cat ctt gtt aca agc tta aaa gga cta tgg aca ctt cgt gcc ttc gga			3339
298	His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly			
299	1055	1060	1065	
301	cgg cag cct tac ttt gaa act ctg ttc cac aaa gct ctg aat tta cat			3387
302	Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His			
303	1070	1075	1080	1085
305	act gcc aac tgg ttc ttg tac ctg tca aca ctg cgc tgg ttc caa atg			3435
306	Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met			
307	1090	1095	1100	
309	aga ata gaa atg att ttt gtc atc ttc att gct gtt acc ttc att			3483
310	Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile			
311	1105	1110	1115	
313	tcc att tta aca aca gga gaa gga gaa aga gtt ggt att atc ctg			3531
314	Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu			
315	1120	1125	1130	
317	act tta gcc atg aat atc atg agt aca ttg cag tgg gct gta aac tcc			3579
318	Thr Leu Ala Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser			
319	1135	1140	1145	
321	agc ata gat gtg gat agc ttg atg cga tct gtg agc cga gtc ttt aag			3627
322	Ser Ile Asp Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys			
W--> 323	1150	1155	1160	1165

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325	ttc att gac atg cca aca gaa ggt aaa cct acc aag tca acc aaa cca	3675
326	Phe Ile Asp Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro	
327	1170 1175 1180	
329	tac aag aat ggc caa ctc tcg aaa gtt atg att att gag aat tca cac	3723
330	Tyr Lys Asn Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His	
331	1185 1190 1195	
333	gtg aag aaa gat gac atc tgg ccc tca ggg ggc caa atg act gtc aaa	3771
334	Val Lys Lys Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys	
335	1200 1205 1210	
337	gat ctc aca gca aaa tac aca gaa ggt gga aat gcc ata tta gag aac	3819
338	Asp Leu Thr Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn	
339	1215 1220 1225	
341	att tcc ttc tca ata agt cct ggc cag agg gtc ggc ctc ttg gga aga	3867
342	Ile Ser Phe Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg	
W--> 343	1230 1235 1240 1245	3915
345	act gga tca ggg aag agt act ttg tta tca gct ttt ttg aga cta ctg	
346	Thr Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu	
347	1250 1255 1260	
349	aac act gaa gga aatc cag atc gat ggt gtc tct ttg gat tca ata	3963
350	Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile	
351	1265 1270 1275	
353	act ttg caa cag tgg agg aaa gcc ttt gga gtc ata cca cag aaa gta	4011
354	Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val	
355	1280 1285 1290	
357	ttt att ttt tct gga aca ttt aga aaa aac ttg gat ccc tat gaa cag	4059
358	Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln	
359	1295 1300 1305	
361	tgg agt gat caa gaa ata tgg aaa gtt gca gat gag gtt ggg ctc aga	4107
362	Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg	
W--> 363	310 1315 1320 1325	4155
365	tct gtg ata gaa cag ttt cct ggg aag ctt gac ttt gtc ctt gtc gat	
366	Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp	
367	1330 1335 1340	
369	ggg ggc tgt gtc cta agc cat ggc cac aag cag ttg atg tgc ttg gct	4203
370	Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala	
371	1345 1350 1355	
373	aga tct gtt ctc agt aag gcg aag atc ttg ctg ctt gat gaa ccc agt	4251
374	Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu Asp Glu Pro Ser	
375	1360 1365 1370	
377	gct cat ttg gat cca gta aca tac caa ata att aga aga act cta aaa	4299
378	Ala His Leu Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys	
379	1375 1380 1385	
381	caa gca ttt gct gat tgc aca gta att ctc tgt gaa cac agg ata gaa	4347
382	Gln Ala Phe Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu	
W--> 383	390 1395 1400 1405	4395
385	gca atg ctg gaa tgc caa caa ttt ttg gtc ata gaa gag aac aaa gtc	
386	Ala Met Leu Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val	
387	1410 1415 1420	
389	cgg cag tac gat tcc atc cag aaa ctg ctg aac gag agg agc ctc ttc	4443

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445 50 55 60
 446 Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg 80
 447 65 70 75 80
 448 Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala 95
 449 85 90 95
 450 Val Gln Pro Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp 110
 451 100 105 110
 452 Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys 125
 453 115 120 125
 454 Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly 140
 455 130 135 140
 456 Leu His His Ile Gly Met Arg Ile Ala Met Phe Ser Leu Ile 160
 457 145 150 155 160
 458 Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser 175
 459 165 170 175
 460 Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp 190
 461 180 185 190
 462 Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val 205
 463 195 200 205
 464 Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe 220
 465 210 215 220
 466 Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu 240
 467 225 230 235 240
 468 Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser 255
 469 245 250 255
 470 Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val 270
 471 260 265 270
 472 Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu 285
 473 275 280 285
 474 Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr 300
 475 290 295 300
 476 Phe Asn Ser Ser Ala Phe Phe Ser Gly Phe Phe Val Val Phe Leu 320
 477 305 310 315 320
 478 Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile 335
 479 325 330 335
 480 Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg 350
 481 340 345 350
 482 Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile 365
 483 355 360 365
 484 Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu 380
 485 370 375 380
 486 Tyr Asn Leu Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe 400
 487 385 390 395 400
 488 Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn 415
 489 405 410 415
 490 Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn 430
 491 420 425 430
 492 Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile 445
 493 435 440 445

RAW SEQUENCE LISTING DATE: 05/09/2000
 PATENT APPLICATION: US/09/405,735 TIME: 11:10:38

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\05092000\I405735.raw

494 Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
 495 450 455 460
 496 Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
 497 465 470 475 480
 498 Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
 499 485 490 495
 500 Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
 501 500 505 510
 502 Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu
 503 515 520 525
 504 Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
 505 530 535 540
 506 Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
 507 545 550 555 560
 508 Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
 509 565 570 575
 510 Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
 511 580 585 590
 512 Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
 513 595 600 605
 514 His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser
 515 610 615 620
 516 Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
 517 625 630 635 640
 518 Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
 519 645 650 655
 520 Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
 521 660 665 670
 522 Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
 523 675 680 685
 524 Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
 525 690 695 700
 526 Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
 527 705 710 715 720
 528 Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
 529 725 730 735
 530 Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
 531 740 745 750
 532 Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
 533 755 760 765
 534 Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
 535 770 775 780
 536 Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
 537 785 790 795 800
 538 Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
 539 805 810 815
 540 Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
 541 820 825 830
 542 Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Trp Asn Thr

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Input Set : A:\Seqlist.txt
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543 835 840 845
544 Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
545 850 855 860
546 Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
547 865 870 875 880
548 Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
549 885 890 895
550 His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser
551 900 905 910
552 Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala
553 915 920 925
554 Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val
555 930 935 940
556 Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro
557 945 950 955 960
558 Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
559 965 970 975
560 Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
561 980 985 990
562 Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val
563 995 1000 1005
564 Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile Val
565 1010 1015 1020
566 Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln Gln Leu
E--> 567 1025 1030 1035 1040
568 Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr His Leu Val
569 1045 1050 1055
570 Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly Arg Gln Pro
571 1060 1065 1070
572 Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His Thr Ala Asn
573 1075 1080 1085
574 Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met Arg Ile Glu
575 1090 1095 1100
576 Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile Ser Ile Leu
E--> 577 1105 1110 1115 1120
578 Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala
579 1125 1130 1135
580 Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp
581 1140 1145 1150
582 Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp
583 1155 1160 1165
584 Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn
585 1170 1175 1180
586 Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys
E--> 587 1185 1190 1195 1200
588 Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr
589 1205 1210 1215
590 Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe
591 1220 1225 1230
591

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000
TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

592 Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
593 1235 1240 1245
594 Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
595 1250 1255 1260
596 Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu Gln
E--> 597 1265 1270 1275 1280
598 Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe Ile Phe
599 1285 1290 1295
600 Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln Trp Ser Asp
601 1300 1305 1310
602 Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg Ser Val Ile
603 1315 1320 1325
604 Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp Gly Gly Cys
605 1330 1335 1340
606 Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala Arg Ser Val
607 1345 1350 1355 1360
E--> 608 Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu
609 1365 1370 1375
610 Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe
611 1380 1385 1390
612 Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu
613 1395 1400 1405
614 Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr
615 1410 1415 1420
616 Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala
E--> 617 1425 1430 1435 1440
618 Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser
619 1445 1450 1455
620 Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Thr Glu
621 1460 1465 1470
622 Glu Glu Val Gln Asp Thr Arg Leu
623 1475 1480

VERIFICATION SUMMARY DATE: 05/09/2000
PATENT APPLICATION: US/09/405,735 TIME: 11:10:39

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, LENGTH:Input:1 Counted:6129
L:430 M:254 E: (42) Number of Bases conflicts Running Total, SEQ ID:2
L:567 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2